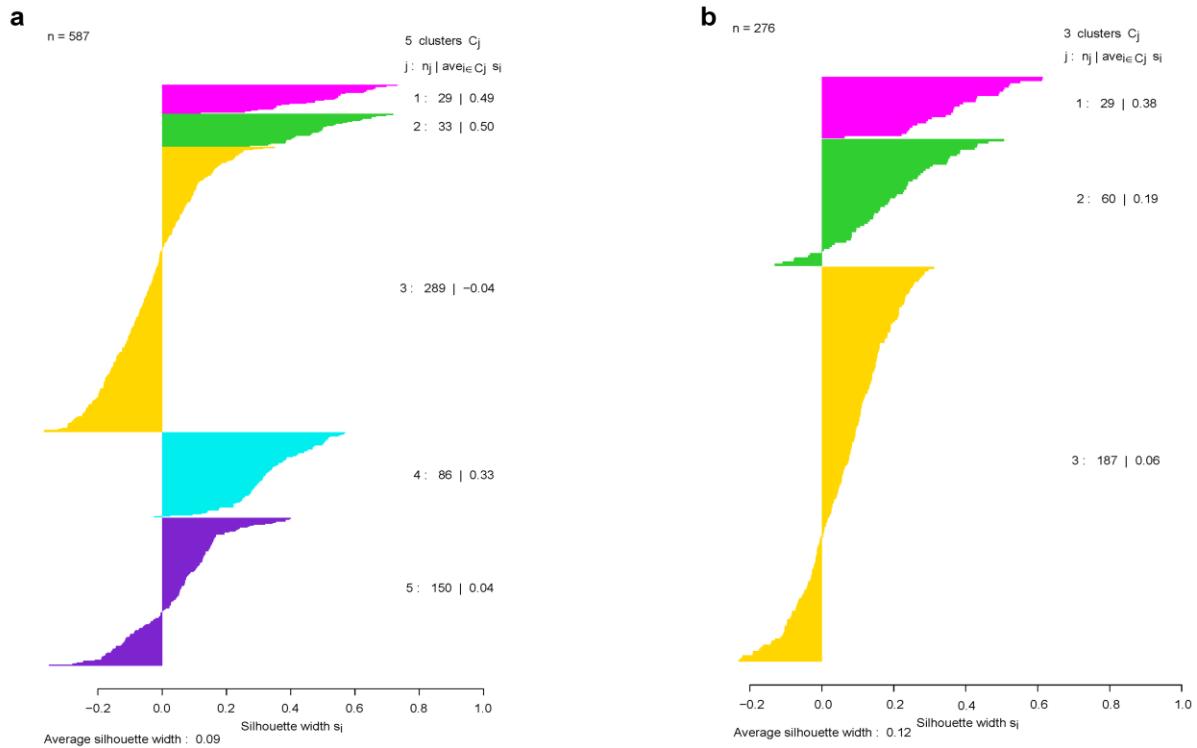
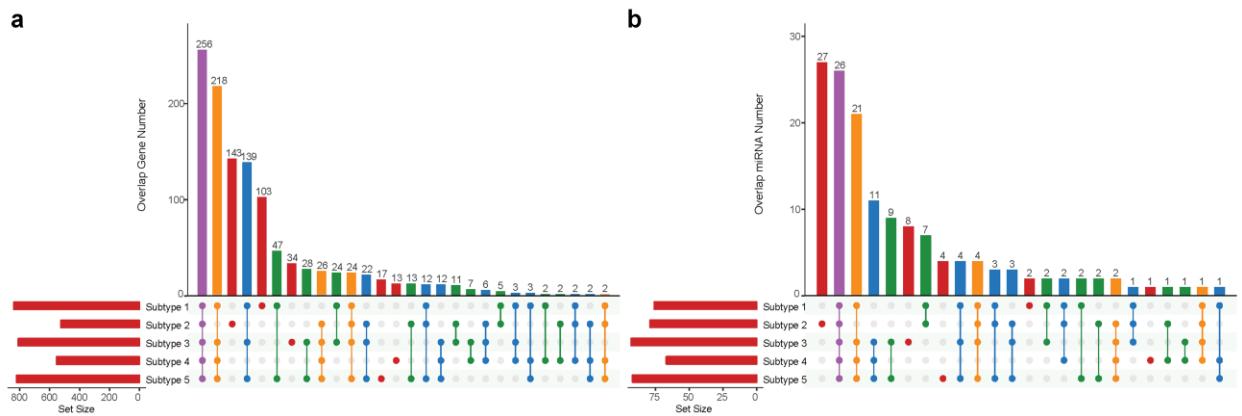


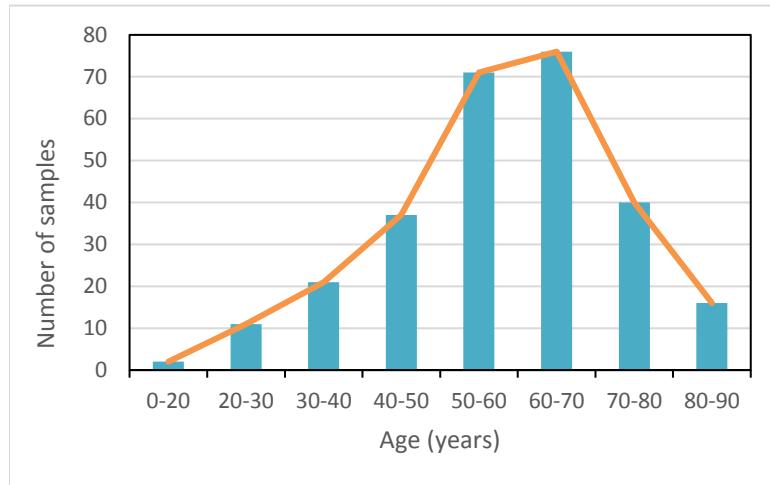
## Additional Figures & Tables



**Figure S1.** Silhouette plots of the identified subtype clusters in clustering. (a) Silhouette plots of subtype clusters in BRCA data. (b) Silhouette plots of subtype clusters in GBM data.



**Figure S2.** Overlaps of the differentially expressed mRNAs and miRNAs in the identified BRCA subtypes. (a) Overlaps of differentially expressed mRNAs in BRCA subtypes; (b) Overlaps of differentially expressed miRNAs in BRCA subtypes.



**Figure S3.** Age distribution of samples in GBM data.

**Table S1.** Cox log rank test p-values of the identified subtypes by using different dimension reduction and data integration parameters in BRCA data.

| PCA explained variance rate | <i>r</i> =0.85 | <i>r</i> =0.90 | <i>r</i> =0.92 | <i>r</i> =0.95 |
|-----------------------------|----------------|----------------|----------------|----------------|
| Integration $\alpha =0.3$   | 7.93e-03       | 1.92e-02       | 2.30e-02       | 2.36e-02       |
| $\alpha =0.4$               | 1.06e-03       | 1.91e-03       | 1.60e-03       | 7.12e-03       |
| $\alpha =0.5$               | 2.10e-02       | 1.79e-02       | 1.03e-02       | 9.26e-03       |
| $\alpha =0.6$               | 3.99e-02       | 9.43e-02       | 5.28e-02       | 7.19e-02       |

**Table S2.** Cox log rank test p-values of the identified subtypes by using different dimension reduction and data integration parameters in GBM data.

| PCA explained variance rate | <i>r</i> =0.85 | <i>r</i> =0.90 | <i>r</i> =0.95 |
|-----------------------------|----------------|----------------|----------------|
| Integration $\alpha =0.3$   | 5.79e-04       | 3.56e-04       | 1.43e-04       |
| $\alpha =0.4$               | 4.00e-04       | 2.86e-04       | 2.51e-04       |
| $\alpha =0.5$               | 1.00e-03       | 1.22e-03       | 1.62e-03       |
| $\alpha =0.6$               | 1.57e-03       | 1.11e-03       | 8.95e-04       |

**Table S3.** Cox log rank test p-values of the identified subtypes by using different data integration and scaling hyper-parameters in BRCA data.

| Parameters  | $\alpha = 0.3$ | $\alpha = 0.4$ | $\alpha = 0.5$ | $\alpha = 0.6$ |
|-------------|----------------|----------------|----------------|----------------|
| $\mu = 0.3$ | 2.30e-02       | 1.60e-03       | 1.03e-02       | 5.28e-02       |
| $\mu = 0.4$ | 6.18e-01       | 6.92e-01       | 4.95e-02       | 5.10e-02       |
| $\mu = 0.5$ | 2.72e-01       | 7.06e-01       | 7.19e-02       | 2.52e-01       |
| $\mu = 0.6$ | 2.84e-01       | 4.11e-01       | 3.62e-01       | 2.07e-01       |
| $\mu = 0.7$ | 3.83e-01       | 2.00e-01       | 1.30e-01       | 2.06e-01       |
| $\mu = 0.8$ | 3.83e-01       | 1.94e-01       | 1.41e-01       | 2.62e-01       |

**Table S4.** Cox log rank test p-values of the identified subtypes by using different data integration and scaling hyper-parameters in GBM data.

| Parameters  | $\alpha = 0.3$ | $\alpha = 0.4$ | $\alpha = 0.5$ | $\alpha = 0.6$ |
|-------------|----------------|----------------|----------------|----------------|
| $\mu = 0.3$ | 1.43e-04       | 2.51e-04       | 1.62e-03       | 8.95e-04       |
| $\mu = 0.4$ | 1.73e-02       | 3.93e-03       | 1.87e-03       | 1.41e-01       |
| $\mu = 0.5$ | 2.18e-02       | 3.24e-03       | 2.00e-03       | 1.76e-01       |
| $\mu = 0.6$ | 3.39e-02       | 1.63e-02       | 1.83e-03       | 1.78e-01       |
| $\mu = 0.7$ | 7.48e-02       | 1.00e-01       | 4.47e-03       | 1.78e-01       |
| $\mu = 0.8$ | 7.48e-02       | 8.50e-02       | 4.15e-03       | 1.78e-01       |